

OLIGODEOXYNUCLEOTIDE Xol26

(SEQ ID NO: 22)

5'-CCCGGGAAGCTT **CCTTAGG** CTTAAAGAAAGTGGTGCTGGGCAAAAAGGG-3'

prepro-HSA \longleftrightarrow V1 domain of CD4 receptor

MstII

OLIGODEOXYNUCLEOTIDE Xol27

(SEQ ID NO: 23)

5'-CCCGGGAAGCTT **TTAGAAAGCTAGCACCACGATGTCTAT**-3'

SmaI HindIII

stop codon

V2 domain of CD4 receptor

Figure 1

(SEQ ID NO. 24)

MstII

CCCTAGGCTTAAAGAAAGTGGTGCTGGGCAAAAAGGGGATACAGTGGAACTGACCTGTACAGCTTCCCAGAAGA
 01 11 21 31 41 51 61 71

AGAGCATACAATTCCACTGGAAAACTCCAACCAGATAAAGATTCTGGGAAATCAGGGCTCCTTCTTAAGTAAAG
 76 86 96 106 116 126 136 146

GTCCATCCAAGCTGAATGATCGCGCTGACTCAAGAAGAAGCCTTTGGGACCAAGGAACTTCCCCCTGATCATCA
 151 161 171 181 191 201 211 221

AGAATCTTAAGATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTGCTAG
 226 236 246 256 266 276 286 296

TGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCTGACCCTGACCTTGGAGAGCCCCC
 301 311 321 331 341 351 361 371

CTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGTAAAAACATACAGGGGGGAAGACCCTCTCCGTGT
 376 386 396 406 416 426 436 446

CTCAGCTGGAGCTCCAGGATAGTGGCACCTGGACATGCACTGTCTTGAGAACCAAGGAAGGTGGAGTTCAAAA
 451 461 471 481 491 501 511 521

HindIII SmaI

TAGACATCGTGGTGCTAGCTTTCTAAAGCTTCCCGGG
 526 536 546 556

Figure 2

(SEQ ID NO. 26)
(SEQ ID NO. 25)

MetLysTrpValThrPheIleSerLeuLeuPheLeuPheSerSerAlaTyrSerArgGlyValPheArg
AAGCTTATGAAGTGGGTAACCTTTATTTCCCTTCTTTTCTCTTTAGCTCGGCTTATTCAGGGGTGTGTTTCGT
1 11 21 31 41 51 61 71
ArgAspAlaHisLysSerGluValAlaHisArgPheLysAspLeuGlyGluGluAsnPheLysAlaLeuValLeu
CGAGATGCACACAAGAGTGAGGTTGCTCATCGGTTTAAAGATTTGGGAGAAGAAAATTTCAAAGCCTTGGTGTTG
76 86 96 106 116 126 136 146
IleAlaPheAlaGlnTyrLeuGlnGlnCysProPheGluAspHisValLysLeuValAsnGluValThrGluPhe
ATTGCCTTTGCTCAGTATCTTCAGCAGTGTCATTGGAAGATCATGTAAAATTAGTGAATGAAGTAAGTGAATTT
151 161 171 181 191 201 211 221
AlaLysThrCysValAlaAspGluSerAlaGluAsnCysAspLysSerLeuHisThrLeuPheGlyAspLysLeu
GCAAAAACATGTGTGCTGATGAGTCAGCTGAAAATTGTGACAAATCACTTCATACCTTTTGGAGACAAATTA
226 236 246 256 266 276 286 296
CysThrValAlaThrLeuArgGluThrTyrGlyGluMetAlaAspCysCysAlaLysGlnGluProGluArgAsn
TGCACAGTTGCAACTCTTCGTGAAACCTATGGTGAAATGGCTGACTGCTGTGCAAAACAAGAACCTGAGAGAAAT
301 311 321 331 341 351 361 371
GluCysPheLeuGlnHisLysAspAspAsnProAsnLeuProArgLeuValArgProGluValAspValMetCys
GAATGCTTCTTGCAACACAAAGATGACAACCCAAACCTCCCCGATTGGTGAGACCAGAGGTTGATGTGATGTGC
376 386 396 406 416 426 436 446
ThrAlaPheHisAspAsnGluGluThrPheLeuLysLysTyrLeuTyrGluIleAlaArgArgHisProTyrPhe
ACTGCTTTTCATGACAATGAAGAGACATTTTTGAAAAATACTTATATGAAATTGCCAGAAGACATCCTTACTTT
451 461 471 481 491 501 511 521
TyrAlaProGluLeuLeuPhePheAlaLysArgTyrLysAlaAlaPheThrGluCysCysGlnAlaAlaAspLys
TATGCCCCGGAACCTCTTTTCTTTGCTAAAAGGTATAAAGCTGCTTTACAGAATGTTGCCAAGCTGCTGATAAA
526 536 546 556 566 576 586 596
AlaAlaCysLeuLeuProLysLeuAspGluLeuArgAspGluGlyLysAlaSerSerAlaLysGlnArgLeuLys
GCTGCCTGCCTGTTGCCAAAGCTCGATGAACTTCGGGATGAAGGAAGGCTTCGTCTGCCAAACAGAGACTCAAG
601 611 621 631 641 651 661 671
CysAlaSerLeuGlnLysPheGlyGluArgAlaPheLysAlaTrpAlaValAlaArgLeuSerGlnArgPhePro
TGTCAGTCTCCAAAAATTTGGAGAAAGAGCTTTCAAAGCATGGGCAGTAGCTCGCCTGAGCCAGAGATTTCCC
676 686 696 706 716 726 736 746
LysAlaGluPheAlaGluValSerLysLeuValThrAspLeuThrLysValHisThrGluCysCysHisGlyAsp
AAAGCTGAGTTTGCAGAAGTTTCCAAGTTAGTGACAGATCTTACCAAAGTCCACACGGAATGCTGCCATGGAGAT
751 761 771 781 791 801 811 821
LeuLeuGluCysAlaAspAspArgAlaAspLeuAlaLysTyrIleCysGluAsnGlnAspSerIleSerSerLys
CTGCTTGAATGTGCTGATGACAGGGCGGACCTTGCCAAGTATATCTGTGAAAATCAAGATTGATCTCCAGTAAA
826 836 846 856 866 876 886 896
LeuLysGluCysCysGluLysProLeuLeuGluLysSerHisCysIleAlaGluValGluAsnAspGluMetPro
CTGAAGGAATGCTGTGAAAAACCTCTGTTGGAAAAATCCCACTGCATTGCCGAAGTGAAAAATGATGAGATGCCT
901 911 921 931 941 951 961 971
AlaAspLeuProSerLeuAlaAlaAspPheValGluSerLysAspValCysLysAsnTyrAlaGluAlaLysAsp
GCTGACTTGCTTCATTAGCTGATTTTGTGAAAGTAAGGATGTTTGCAAAAATATGCTGAGGCAAGGAT
976 986 996 1006 1016 1026 1036 1046

Figure 8A

ValPheLeuGlyMetPheLeuTyrGluTyrAlaArgArgHisProAspTyrSerValValLeuLeuLeuArgLeu
 GTCTTCCTGGGCATGTTTTGTATGAATATGCAAGAAGGCATCCTGATTACTCTGTCGTACTGCTGCTGAGACTT
 1051 1061 1071 1081 1091 1101 1111 1121

AlaLysThrTyrGluThrThrLeuGluLysCysCysAlaAlaAlaAspProHisGluCysTyrAlaLysValPhe
 GCCAAGACATATGAAACCACTCTAGAGAAGTGCTGTGCCGCTGCAGATCCTCATGAATGCTATGCCAAAGTGTTC
 1126 1136 1146 1156 1166 1176 1186 1196

AspGluPheLysProLeuValGluGluProGlnAsnLeuIleLysGlnAsnCysGluLeuPheGluGlnLeuGly
 GATGAATTTAAACCTCTTGTGGAAGAGCCTCAGAATTTAATCAAAACAAAATTGTGAGCTTTTTGAGCAGCTTGA
 1201 1211 1221 1231 1241 1251 1261 1271

GluTyrLysPheGlnAsnAlaLeuLeuValArgTyrThrLysLysValProGlnValSerThrProThrLeuVal
 GAGTACAAATTCAGAATGCGCTATTAGTTCGTTACACCAAGAAAGTACCCCAAGTGTCAACTCCAACCTCTGTA
 1276 1286 1296 1306 1316 1326 1336 1346

GluValSerArgAsnLeuGlyLysValGlySerLysCysCysLysHisProGluAlaLysArgMetProCysAla
 GAGGTCTCAAGAAACCTAGGAAAAGTGGGCAGCAAATGTTGTAAACATCCTGAAGCAAAAAGAAATGCCCTGTGCA
 1351 1361 1371 1381 1391 1401 1411 1421

GluAspTyrLeuSerValValLeuAsnGlnLeuCysValLeuHisGluLysThrProValSerAspArgValThr
 GAAGACTATCTATCCGTGGTCTGAACCAAGTTATGTGTGTTGCATGAGAAAACGCCAGTAAGTGACAGAGTCACC
 1426 1436 1446 1456 1466 1476 1486 1496

LysCysCysThrGluSerLeuValAsnArgArgProCysPheSerAlaLeuGluValAspGluThrTyrValPro
 AAATGCTGCACAGAATCCTTGGTGAACAGGCGACCATGCTTTTCAGCTCTGGAAGTCCGATGAAACATACGTTCCC
 1501 1511 1521 1531 1541 1551 1561 1571

LysGluPheAsnAlaGluThrPheThrPheHisAlaAspIleCysThrLeuSerGluLysGluArgGlnIleLys
 AAAGAGTTTAAATGCTGAAACATTCACCTTCCATGCAGATATATGCACACTTTCTGAGAAGGAGAGACAAATCAAG
 1576 1586 1596 1606 1616 1626 1636 1646

LysGlnThrAlaLeuValGluLeuValLysHisLysProLysAlaThrLysGluGlnLeuLysAlaValMetAsp
 AAACAACTGCACCTTGTGAGCTTGTGAAACACAAGCCCAAGGCAACAAAGAGCAACTGAAAGCTGTTATGGAT
 1651 1661 1671 1681 1691 1701 1711 1721

AspPheAlaAlaPheValGluLysCysCysLysAlaAspAspLysGluThrCysPheAlaGluGluGlyLysLys
 GATTTCCGAGCTTTGTAGAGAAGTGCTGCAAGGCTGACGATAAGGAGACCTGCTTTGCCGAGGAGGGTAAAAAA
 1726 1736 1746 1756 1766 1776 1786 1796

LeuValAlaAlaSerGlnAlaAlaLeuGlyLeuLysLysValValLeuGlyLysLysGlyAspThrValGluLeu
 CTTGTTGCTGCAAGTCAAGCTGCCTTAGGCTTAAAGAAAGTGGTGCTGGGCAAAAAGGGGATACAGTGGAACTG
 1801 1811 1821 1831 1841 1851 1861 1871

ThrCysThrAlaSerGlnLysLysSerIleGlnPheHisTrpLysAsnSerAsnGlnIleLysIleLeuGlyAsn
 ACCTGTACAGCTTCCCAGAAGAAGAGCATACAATCCACTGGAAAACTCCAACCAGATAAAGATTCTGGGAAAT
 1876 1886 1896 1906 1916 1926 1936 1946

GlnGlySerPheLeuThrLysGlyProSerLysLeuAsnAspArgAlaAspSerArgArgSerLeuTrpAspGln
 CAGGGCTCCTTCTTAACATAAGGTCCATCCAAGCTGAATGATCGCGCTGACTCAAGAAGAAGCCTTTGGGACCAA
 1951 1961 1971 1981 1991 2001 2011 2021

GlyAsnPheProLeuIleIleLysAsnLeuLysIleGluAspSerAspThrTyrIleCysGluValGluAspGln
 GGAAACTTCCCCCTGATCATCAAGAATCTTAAGATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAG
 2026 2036 2046 2056 2066 2076 2086 2096

LysGluGluValGlnLeuLeuValPheGlyLeuThrAlaAsnSerAspThrHisLeuLeuGlnGlyGlnSerLeu
 AAGGAGGAGGTGCAATTGCTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCTG
 2101 2111 2121 2131 2141 2151 2161 2171

Figure 8B

ThrLeuThrLeuGluSerProProGlySerSerProSerValGlnCysArgSerProArgGlyLysAsnIleGln
 ACCCTGACCTTGGAGAGCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGTAAAAACATACAG
 2176 2186 2196 2206 2216 2226 2236 2246

 GlyGlyLysThrLeuSerValSerGlnLeuGluLeuGlnAspSerGlyThrTrpThrCysThrValLeuGlnAsn
 GGGGGGAAGACCCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGCACCTGGACATGCACTGTCTTGCAAGAC
 2251 2261 2271 2281 2291 2301 2311 2321

 GlnLysLysValGluPheLysIleAspIleValValLeuAlaPhe***
 CAGAAGAAGGTGGAGTTCAAAATAGACATCGTGGTGCTAGCTTTCTAAAAGCTT
 2326 2336 2346 2356 2366 2376

Figure 8C

(SEQ ID No. 28)
(SEQ ID No. 29)

R S L E R I A R (L) E E K V K T
5' AGATCTTTGGAAAGAATTGCCCGTCTGGAAGAAAAAGTGAAAAC
BglII

(L) K A Q N S E (L) A S T A N M (L)
CTGAAAGCCCGAGAACTCTGAGCTCGCATCCACGGCCAACATGCTG

R E Q V A Q (L) K Q L V G D A
CGTGAACAGGTTGCACAGCTGAAGCAACTGGTTGGCGACGCC 3'
AhaII



Figure 34

a

b

Cys Phe Ser Ala Leu Glu Val Asp **Glu** Thr Tyr Val =====

(SEQ ID NO. 29)

• BAL31 DELETION (YP63)

Cys Phe Ser Ala Leu Glu Val Asp Ala Leu Gly =====

(SER ID. No. 31)

HSA

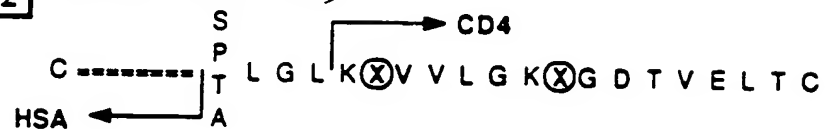
Mestil

Figure 36

1 (SEQ ID No. 33)



2 (SEQ ID No. 34)



3 (SEQ ID No. 35)



4

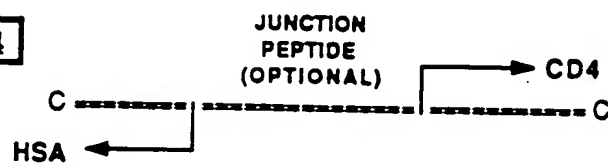


Figure 37

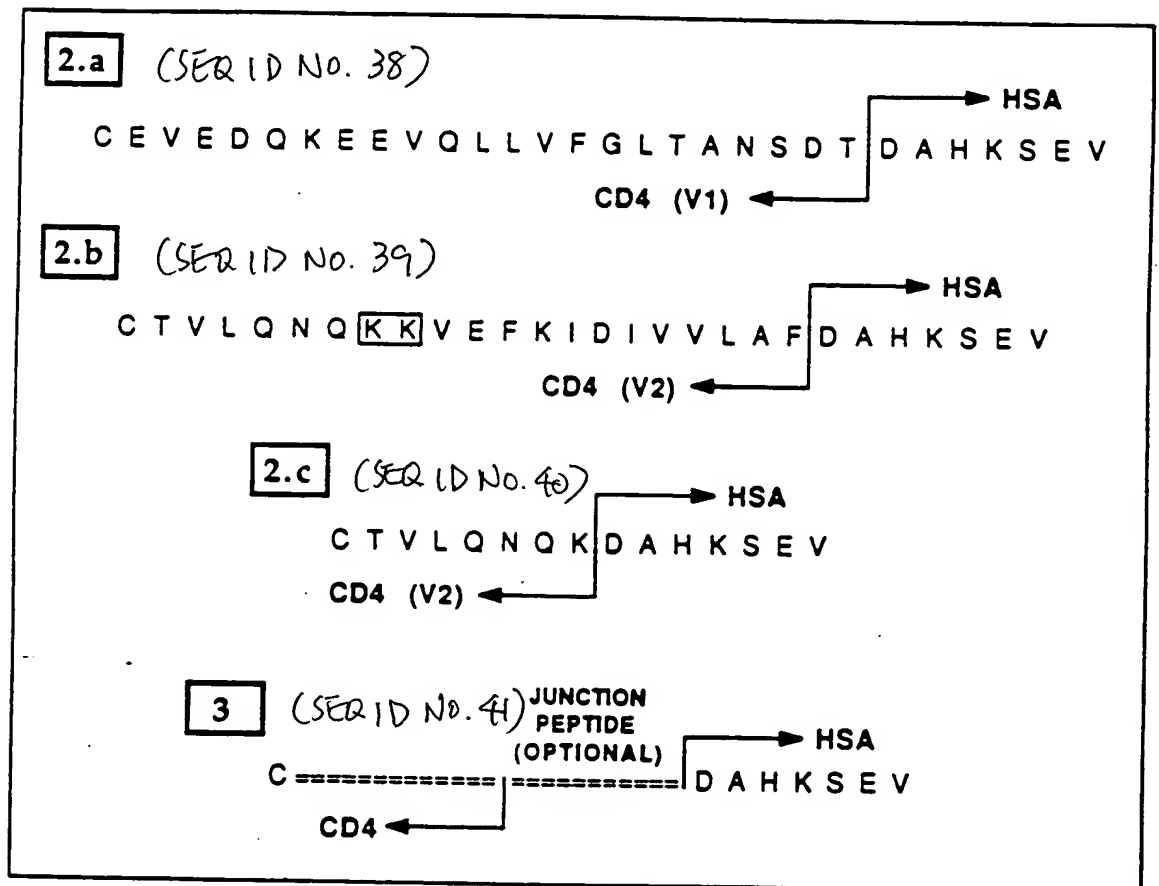
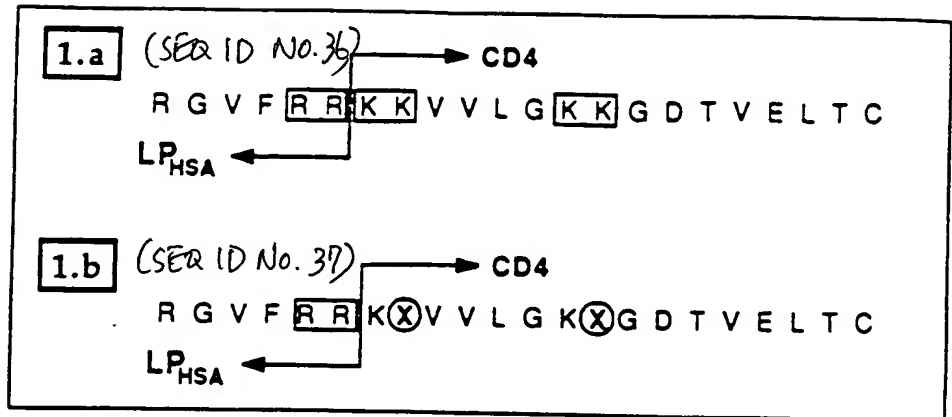


Figure 38